

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1. – 58. (Cancelled).

59. (Currently amended) A method for detecting a human metapneumovirus in a sample, wherein the method comprises contacting the sample with a nucleic acid encoding an amino acid sequence that is:

- ~~(a) an amino acid sequence that is greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1, SEQ ID NO.: 1 or 99-1 as shown in Figure 20;~~
- ~~(b) an amino acid sequence that is greater than 68% identical to the amino acid sequence of the P protein of MPV isolate 00-1 or 99-1 as shown in Figure 21;~~
- ~~(c) an amino acid sequence that is greater than 87% identical to the amino acid sequence of the M protein of MPV isolate 00-1 or 99-1 as shown in Figure 22;~~
- ~~(d) an amino acid sequence that is greater than 81% identical to the amino acid sequence of the F protein of MPV isolate 00-1 or 99-1 as shown in Figure 23;~~
- ~~(e) an amino acid sequence that is greater than 84% identical to the amino acid sequence of the M2-1 protein of MPV isolate 00-1 or 99-1 as shown in Figure 24;~~
- ~~(f) an amino acid sequence that is greater than 56% identical to the amino acid sequence of the M2-2 protein of MPV isolate 00-1 or 99-1 as shown in Figure 25;~~
- ~~(g) an amino acid sequence that is greater than 90% identical to the amino acid sequence of the L protein of MPV isolate 00-1 or 99-1 as shown in Figure 28;~~
- ~~(h) an amino acid sequence that is greater than 29% identical to the amino acid sequence of the SH protein of MPV isolate 00-1 or 99-1 as shown in Figure 26; or~~
- ~~(i) an amino acid sequence that is greater than 29% identical to the amino acid sequence of the G protein of MPV isolate 00-1 or 99-1 as shown in Figure 27.~~

60. (Currently amended) A method for detecting a human metapneumovirus in a sample, wherein the method comprises contacting the sample with an antibody that specifically binds to a protein that is:

- (a) greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1, SEQ ID NO.: 1 or 99-1 as shown in Figure 20;
- (b) greater than 68% identical to the amino acid sequence of the P protein of MPV isolate 00-1 or 99-1 as shown in Figure 21;
- (c) greater than 87% identical to the amino acid sequence of the M protein of MPV isolate 00-1 or 99-1 as shown in Figure 22;
- (d) greater than 81 % identical to the amino acid sequence of the F protein of MPV isolate 00-1 or 99-1 as shown in Figure 23;
- (e) greater than 84% identical to the amino acid sequence of the M2-1 protein of MPV isolate 00-1 or 99-1 as shown in Figure 24;
- (f) greater than 56% identical to the amino acid sequence of the M2-2 protein of MPV isolate 00-1 or 99-1 as shown in Figure 25;
- (g) greater than 90% identical to the amino acid sequence of the L protein of MPV isolate 00-1 or 99-1 as shown in Figure 28;
- (h) greater than 29% identical to the amino acid sequence of the SH protein of MPV isolate 00-1 or 99-1 as shown in Figure 26; or
- (i) greater than 29% identical to the amino acid sequence of the G protein of MPV isolate 00-1 or 99-1 as shown in Figure 27.

61. (Currently amended) A method for detecting a human metapneumovirus in a sample, wherein the method comprises contacting the sample with a first group of one or more nucleic acids that hybridize under stringent conditions to a second group of one or more nucleic acids, that encodes a protein, or fragment thereof, ~~comprising~~, consisting of

- ~~(a) a sequence that is greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1, SEQ ID NO.: 1 and 99-1 as shown in figure 20;~~
- ~~(b) a sequence that is greater than 68% identical to the amino acid sequence of ——— the P protein of MPV isolate 00-1 and 99-1 as shown in figure 21;~~
- ~~(c) a sequence that is greater than 87% identical to the amino acid sequence of ——— the M protein of MPV isolate 00-1 and 99-1 as shown in figure 22;~~
- ~~(d) a sequence that is greater than 81% identical to the amino acid sequence of ——— the F protein of MPV isolate 00-1 and 99-1 as shown in figure 23;~~

- ~~(e) a sequence that is greater than 84% identical to the amino acid sequence of~~
~~the M2-1 protein of MPV isolate 00-1 and 99-1 as shown in figure 24;~~
- ~~(f) a sequence that is greater than 56% identical to the amino acid sequence of~~
~~the M2-2 protein of MPV isolate 00-1 and 99-1 as shown in figure 25;~~
- ~~(g) a sequence that is greater than 90% identical to the amino acid sequence of~~
~~the L protein of MPV isolate 00-1 and 99-1 as shown in figure 28;~~
- ~~(h) a sequence that is greater than 29% identical to the amino acid sequence of~~
~~the SH protein of MPV isolate 00-1 and 99-1 as shown in figure 26; or~~
- ~~(i) a sequence that is greater than 29% identical to the amino acid sequence of~~
~~the G protein of MPV isolate 00-1 and 99-1 as shown in figure 27;~~
~~wherein sequence identity is determined over the entire length of the protein.~~

62. (Currently amended) A method for detecting a human metapneumovirus in a sample, wherein the method comprises contacting the sample with one or more nucleic acids that hybridize under stringent conditions to the genome or antigenome of the virus isolate deposited as I-2614 with CNCM, Paris.

63. (Currently amended) The method of claim 59, wherein the amino acid is:

- ~~(i) SEQ ID No.: 64 or 98;~~
- ~~(ii) SEQ ID No.: 21 or 94;~~
- ~~(iii) SEQ ID No.: 99 or 100;~~
- ~~(iv) SEQ ID No.: 47 or 95;~~
- ~~(v) SEQ ID No.: 55 or 96;~~
- ~~(vi) SEQ ID No.: 14 or 93;~~
- ~~(vii) SEQ ID No.: 1 or 91;~~
- ~~(viii) SEQ ID No.: 8 or 92; or~~
- ~~(ix) SEQ ID No.: 63 or 97.~~

64. (Cancelled).

65. (Cancelled).

66. (Currently amended) The method of claim 60, wherein the protein consists of an amino acid sequence of:

- ~~(i) SEQ ID No.: 64 or 98;~~

- ~~(ii) — SEQ ID No.: 21 or 94;~~
- ~~(iii) — SEQ ID No.: 99 or 100;~~
- ~~(iv) — SEQ ID No.: 47 or 95;~~
- ~~(v) — SEQ ID No.: 55 or 96;~~
- ~~(vi) — SEQ ID No.: 14 or 93;~~
- ~~(vii) — SEQ ID No.: 1 or 91;~~
- ~~(viii) — SEQ ID No.: 8 or 92; or~~
- ~~(ix) — SEQ ID No.: 63 or 97.~~

67. (Previously presented) The method of claim 66, wherein the method further comprises an immune fluorescence assay.

68. (Currently amended) A method for detecting an antibody against human metapneumovirus in a sample, wherein the method comprises contacting the sample with a protein comprising the amino acid sequence of:

- ~~(vii) — SEQ ID No.: 64 or 98;~~
- ~~(viii) — SEQ ID No.: 21 or 94;~~
- ~~(ix) — SEQ ID No.: 99 or 100;~~
- ~~(x) — SEQ ID No.: 47 or 95;~~
- ~~(xi) — SEQ ID No.: 55 or 96;~~
- ~~(xii) — SEQ ID No.: 14 or 93;~~
- ~~(vii) — SEQ ID No.: 1 or 91;~~
- ~~(viii) — SEQ ID No.: 8 or 92; or~~
- ~~(ix) — SEQ ID No.: 63 or 97.~~

69. (New) The method of claim 59 or 62, wherein the nucleic acid is at least 90% identical to SEQ ID No.:1.